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Sequence Listing was accepted with existing errors.

See attached Validation Report.

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Reviewer: MSpencer

Timestamp: Mon May 07 12:02:37 EDT 2007

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Application No: 10573245 Version No: 1.0

Input Set:

Output Set:

Started: 2007-04-20 12:00:24.452
Finished: 2007-04-20 12:00:24.973
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 521 ms
Total Warnings: 1
Total Errors: 1
No. of SeqIDs Defined: 24
Actual SeqID Count: 24

ErrCode **Error Description**

E 320	Wrong Nucleic Acid Designator, gab in SEQID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (8)

SEQUENCE LISTING

<110> The University of York

<120> Expansion Polypeptides

<130> 2902076.1

<140> 10573245

<141> 2007-05-07

<150> 10/573,245

<151> 2006-03-23

<150> PCT/GB04/04058

<151> 2004-08-23

<160> 24

<170> PatentIn version 3.4

<210> 1

<211> 783

<212> DNA

<213> Craterostigma plantagineum

<220>

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<222> (1)..(783)

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acc agc agc agc cat ttt gcg cgc gcg tat tat ggc ggc gat ggc ggc 96
Thr Ser Ser Ser His Phe Ala Arg Ala Tyr Tyr Gly Gly Asp Gly Gly
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tgg acc gat gcg cat gcg acc ttt tat ggc ggc agc gat gcg agc ggc 144
Trp Thr Asp Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly
35 40 45

acc atg ggc ggc gcg tgc ggc tat ggc aac ctg tat agc cag ggc tat 192
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ggc acc aac acc gcg gcg ctg agc acc gcg ctg ttt aac aac ggc ctg 240
Gly Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu
65 70 75 80

agc tgc ggc agc tgc ttt gaa att aaa tgc gcg agc agc att agc ggc 288
Ser Cys Gly Ser Cys Phe Glu Ile Lys Cys Ala Ser Ser Ile Ser Gly
85 90 95

ggc ggc aaa tgg tgc ctg ccg ggc ggc agc att acc gtc acc gcg acc		336	
Gly Gly Lys Trp Cys Leu Pro Gly Gly Ser Ile Thr Val Thr Ala Thr			
100	105	110	
aac ttt tgc ccg ccg aac aac gcg ctg ccg aac aac gcg ggc ggc tgg		384	
Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn Asn Ala Gly Gly Trp			
115	120	125	
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Cys Asn Pro Pro Leu Gln His Phe Asp Leu Ser Gln Pro Val Phe Gln			
130	135	140	
cat att gcg cag tat cgc gcg ggc att gtc ccg gtc agc tat cgc cgc		480	
His Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Tyr Arg Arg			
145	150	155	160
gtg ccg tgc cgc cgc ggc ggc att cgc ttt acc att aac ggc cat		528	
Val Pro Cys Arg Arg Gly Gly Ile Arg Phe Thr Ile Asn Gly His			
165	170	175	
agc tat ttt aac ctg gtc ctg att acc aac gtc ggc ggc gtc gat		576	
Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp			
180	185	190	
gtg cat gcg gtc agc att aaa ggc gcg acc acc gat tgg cag ccg atg		624	
Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met			
195	200	205	
agc cgc aac tgg ggc cag aac tgg cag agc aac gcg aac ccg aac ggc		672	
Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Ala Asn Pro Asn Gly			
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Gln Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val			
225	230	235	240
agc aac aac gtc gcg ccg aac tgg agc ttt ggc cag acc ttt gcg		768	
Ser Asn Asn Val Ala Pro Pro Asn Trp Ser Phe Gly Gln Thr Phe Ala			
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20

25

30

Trp Thr Asp Ala His Ala Thr Phe Tyr Gly Gly Ser Asp Ala Ser Gly
35 40 45

Thr Met Gly Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr
50 55 60

Gly Thr Asn Thr Ala Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu
65 70 75 80

Ser Cys Gly Ser Cys Phe Glu Ile Lys Cys Ala Ser Ser Ile Ser Gly
85 90 95

Gly Gly Lys Trp Cys Leu Pro Gly Gly Ser Ile Thr Val Thr Ala Thr
100 105 110

Asn Phe Cys Pro Pro Asn Asn Ala Leu Pro Asn Asn Ala Gly Gly Trp
115 120 125

Cys Asn Pro Pro Leu Gln His Phe Asp Leu Ser Gln Pro Val Phe Gln
130 135 140

His Ile Ala Gln Tyr Arg Ala Gly Ile Val Pro Val Ser Tyr Arg Arg
145 150 155 160

Val Pro Cys Arg Arg Arg Gly Gly Ile Arg Phe Thr Ile Asn Gly His
165 170 175

Ser Tyr Phe Asn Leu Val Leu Ile Thr Asn Val Gly Gly Ala Gly Asp
180 185 190

Val His Ala Val Ser Ile Lys Gly Ala Thr Thr Asp Trp Gln Pro Met
195 200 205

Ser Arg Asn Trp Gly Gln Asn Trp Gln Ser Asn Ala Asn Pro Asn Gly
210 215 220

Gln Arg Leu Ser Phe Lys Val Thr Thr Ser Asp Gly Arg Thr Leu Val
225 230 235 240

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Gly Ala Gln Phe Asn

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48

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Cys Gly Tyr Gly Asn Leu Tyr Ser Thr Gly Tyr Gly Thr Asn Thr Ala
20 25 30

96

gct ctg agc acc gct ctg ttt aac aac ggc ctg acc tgc ggc gct tgc
Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Thr Cys Gly Ala Cys
35 40 45

144

tat gaa ctg acc tgc aac aac gat ccg cgc ggc tgg tgc ctg agc ggc
Tyr Glu Leu Thr Cys Asn Asn Asp Pro Arg Gly Trp Cys Leu Ser Gly
50 55 60

192

acc att atg gtg acc gct acc aac ttt tgc ccg ccg aac ccg agc ctg
Thr Ile Met Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Pro Ser Leu
65 70 75 80

240

ccg aac gat aac ggc ggc tgg tgc aac ccg ccg cgc cag cat ttt gat
Pro Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg Gln His Phe Asp
85 90 95

288

ctg gct gaa ccg gct ttt ctg cag att gct cag tat aaa gct ggc att
Leu Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Lys Ala Gly Ile
100 105 110

336

gtg ccg gtg aac tat cgc cgc gtg ccg tgc cag aaa aaa ggc ggc att
Val Pro Val Asn Tyr Arg Arg Val Pro Cys Gln Lys Lys Gly Gly Ile
115 120 125

384

cgc ttt acc att aac ggc cat agc ttt ttt aac ctg gtg ctg gtg acc
Arg Phe Thr Ile Asn Gly His Ser Phe Phe Asn Leu Val Leu Val Thr
130 135 140

432

aac gtg ggc ggc gtg ggc gat gtg cat agc gtg agc att aaa ggc agc
Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser
145 150 155 160

480

aac ggc ggc tgg cag ccg ctg agc cgc aac tgg ggc cag aac tgg cag 528
Asn Gly Gly Trp Gln Pro Leu Ser Arg Asn Trp Gly Gln Asn Trp Gln
165 170 175

agc aac agc tat ctg aac ggc cag agc ctg agc ttt cag gtg acc acc 576
Ser Asn Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Gln Val Thr Thr
180 185 190

agc gat ggc cgc acc gtg acc agc tat gat gtg gcg ccg cgc ggc tgg 624
Ser Asp Gly Arg Thr Val Thr Ser Tyr Asp Val Ala Pro Arg Gly Trp
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cag ttt ggc cag acc ttt gaa ggc ggc cag ttt 657
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<213> Craterostigma plantagineum

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Ala Leu Ser Thr Ala Leu Phe Asn Asn Gly Leu Thr Cys Gly Ala Cys
35 40 45

Tyr Glu Leu Thr Cys Asn Asn Asp Pro Arg Gly Trp Cys Leu Ser Gly
50 55 60

Thr Ile Met Val Thr Ala Thr Asn Phe Cys Pro Pro Asn Pro Ser Leu
65 70 75 80

Pro Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg Gln His Phe Asp
85 90 95

Leu Ala Glu Pro Ala Phe Leu Gln Ile Ala Gln Tyr Lys Ala Gly Ile
100 105 110

Val Pro Val Asn Tyr Arg Arg Val Pro Cys Gln Lys Lys Gly Gly Ile
115 120 125

Arg Phe Thr Ile Asn Gly His Ser Phe Phe Asn Leu Val Leu Val Thr

130	135	140	
Asn Val Gly Gly Val Gly Asp Val His Ser Val Ser Ile Lys Gly Ser			
145	150	155	160
Asn Gly Gly Trp Gln Pro Leu Ser Arg Asn Trp Gly Gln Asn Trp Gln			
165	170	175	
Ser Asn Ser Tyr Leu Asn Gly Gln Ser Leu Ser Phe Gln Val Thr Thr			
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ggc gcg tgc ggc tat ggc aac ctg tat agc cag ggc tat ggc acc aac 96			
Gly Ala Cys Gly Tyr Gly Asn Leu Tyr Ser Gln Gly Tyr Gly Thr Asn			
20	25	30	
acc gcg gcg ctg agc acc acc ctg ttt aac aac ggc ctg gcg tgc ggc 144			
Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly			
35	40	45	
agc tgc tat cag gtg cgc tgc gaa ggc ggc ccg aaa tgg tgc gtg cgc 192			
Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg			
50	55	60	
ggc ggc gat cgc att att acc gtg acc gcg acc aac ttt tgc ccg ccg 240			
Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro			
65	70	75	80
aac tat gcg ctg gcg aac gat aac ggc ggc tgg tgc aac ccg ccg cgc 288			
Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg			
85	90	95	

cag cat ttt gat atg gcg cag ccg gcg ttt gtg cgc att gcg cat tat			336
Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr			
100	105	110	
cgc gcg ggc att gtg ccg att agc tat cgc cgc gtg agc tgc gtg aaa			384
Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys			
115	120	125	
aaa ggc ggc att cgc ctg acc att aac ggc cat agc tat ttt aac ctg			432
Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu			
130	135	140	
gtg ctg gtg agc aac gtg ggc agc ggc gat gtg cat gcg gtg tgg			480
Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp			
145	150	155	160
att aaa ggc agc ggc ggc ccg tgg cag gcg atg acc cgc aac tgg			528
Ile Lys Gly Ser Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp			
165	170	175	
ggc cag aac tgg cag agc aac agc tat ctg gat ggc cag agc ctg agc			576
Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser			
180	185	190	
ttt att gtg cgc gcg ggc gat ggc cgc acc gtg acc gcg aac gab att			624
Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Xaa Ile			
195	200	205	
gtg ccg cgc ggc tgg cag ttt ggc cag acc ttt gaa ggc ccg cag ttt			672
Val Pro Arg Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Pro Gln Phe			
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 20 25 30

Thr Ala Ala Leu Ser Thr Thr Leu Phe Asn Asn Gly Leu Ala Cys Gly
 35 40 45

Ser Cys Tyr Gln Val Arg Cys Glu Gly Gly Pro Lys Trp Cys Val Arg
50 55 60

Gly Gly Asp Arg Ile Ile Thr Val Thr Ala Thr Asn Phe Cys Pro Pro
65 70 75 80

Asn Tyr Ala Leu Ala Asn Asp Asn Gly Gly Trp Cys Asn Pro Pro Arg
85 90 95

Gln His Phe Asp Met Ala Gln Pro Ala Phe Val Arg Ile Ala His Tyr
100 105 110

Arg Ala Gly Ile Val Pro Ile Ser Tyr Arg Arg Val Ser Cys Val Lys
115 120 125

Lys Gly Gly Ile Arg Leu Thr Ile Asn Gly His Ser Tyr Phe Asn Leu
130 135 140

Val Leu Val Ser Asn Val Gly Gly Ser Gly Asp Val His Ala Val Trp
145 150 155 160

Ile Lys Gly Ser Gly Gly Pro Trp Gln Ala Met Thr Arg Asn Trp
165 170 175

Gly Gln Asn Trp Gln Ser Asn Ser Tyr Leu Asp Gly Gln Ser Leu Ser
180 185 190

Phe Ile Val Arg Ala Gly Asp Gly Arg Thr Val Thr Ala Asn Xaa Ile
195 200 205

Val Pro Arg Gly Trp Gln Phe Gly Gln Thr Phe Glu Gly Pro Gln Phe
210 215 220

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<210> 8

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<220>
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<222> (2)..(2)
<223> s is Guanine or cytosine

<220>
<221> misc_feature
<222> (3)..(3)
<223> n is a, c, g, or t

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<222> (6)..(6)
<223> y is pyrimidine

<220>
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<222> (9)..(9)
<223> n is a, c, g, or t

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<2